



1	ATG	GCT	GGA	CCT	GCC	ACC	CAG	AGC	CCC	ATG	AAG	CTG	ATG	GCC	CTG	45
46	CAG	CTG	CTG	CTG	TGG	AGT	GCA	CTC	TGG	ACA	GTG	CAG	GAA	GCC	ACC	90
91	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	CTC	AAG	135
136	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	GCG	CTC	180
181	CAG	GAG	AAG	CTG	GCA	GGC	TGC	TTG	AGC	CAA	CTC	CAT	AGC	GGC	CTT	225
226	TTC	CTC	TAC	CAG	GGG	CTC	CTG	CAG	GCC	CTG	GAA	GGG	ATC	TCC	CCC	270
271	GAG	TTG	GGT	CCC	ACC	TTG	GAC	ACA	CTG	CAG	CTG	GAC	GTC	GCC	GAC	315
316	TTT	GCC	ACC	ACC	ATC	TGG	CAG	CAG	ATG	GAA	GAA	CTG	GGA	ATG	GCC	360
361	CCT	GCC	CTG	CAG	CCC	ACC	CAG	GGT	GCC	ATG	CCG	GCC	TTC	GCC	TCT	405
406	GCT	TTC	CAG	CGC	CGG	GCA	GGA	GGG	GTC	CTA	GTT	GCC	TCC	CAT	CTG	450
451	CAG	AGC	TTC	CTG	GAG	GTG	TCG	TAC	CGC	GTT	CTA	CGC	CAC	CTT	GCC	495
496	CAG	CCC	TAA	TAA												508

(see: SEQ ID NO: 17)

stop codon

FIG. 1

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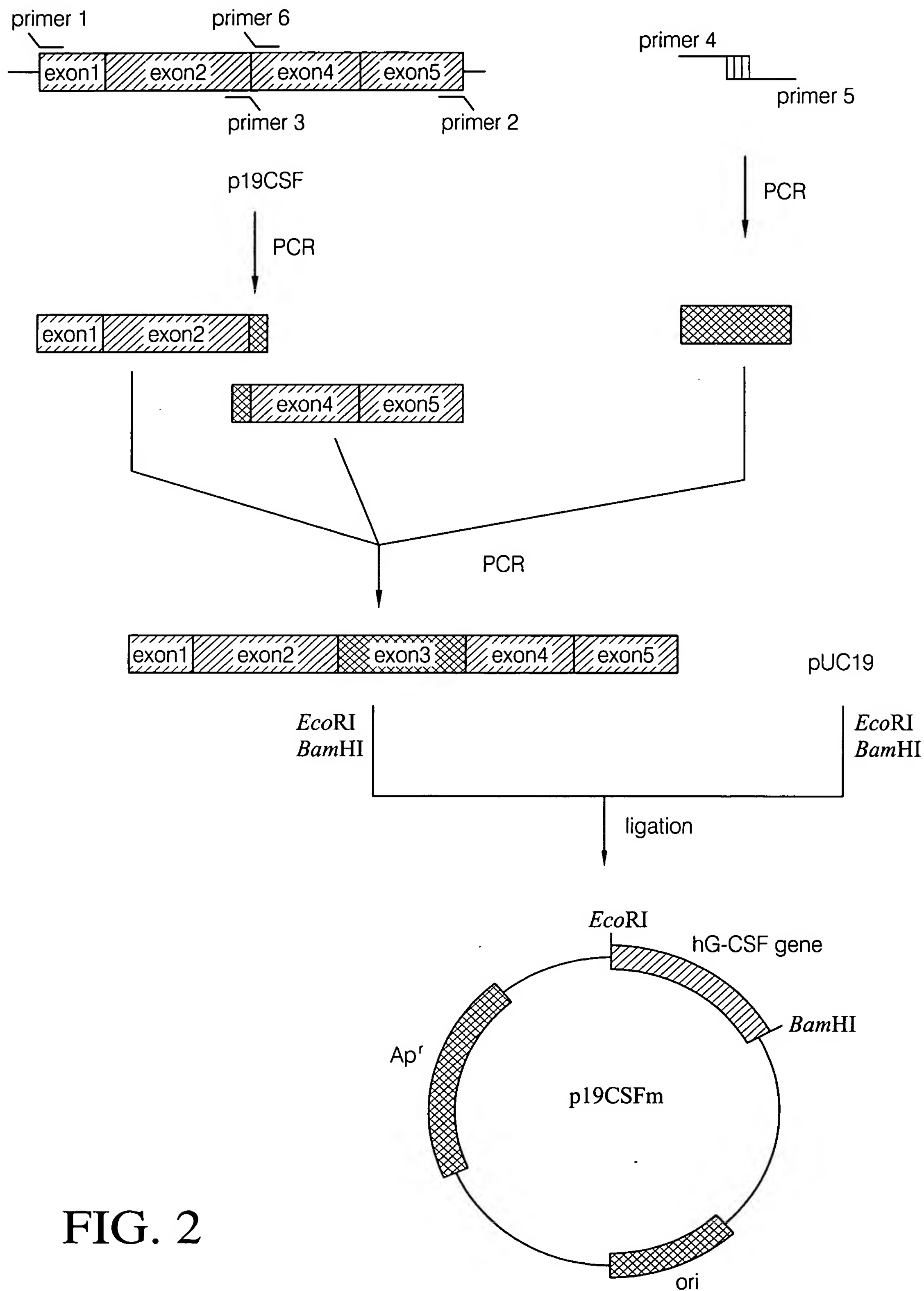


FIG. 2

ESCHERICHIA COLI STRAIN SECRETING HUMAN GRANULOCYTE...

Sang-Yup Lee

Appl. No.: 10/009,792 Atty Docket: HYLEE60.001APC

Replacement Sheet

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	-30															-16	
1	ATG	GCT	GGA	CCT	GCC	ACC	CAG	AGC	CCC	ATG	AAG	CTG	ATG	GCC	CTG	45	
	-15															-1	+1
46	CAG	CTG	CTG	CTG	TGG	AGT	GCA	CTC	TGG	ACA	GTG	CAG	GAA	GCC	ACC	90	Thr
	2															16	
91	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	CTC	AAG	135	Lys
	17															31	
136	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	GCG	CTC	180	Leu
	32															46	
181	CAG	GAG	AAG	CTG	TGT	GCC	ACC	TAC	AAG	CTG	TGC	CAC	CCC	GAG	GAG	225	Glu
	47															61	
226	CTG	GTG	CTG	CTC	GGA	CAC	TCT	CTG	GGC	ATC	CCC	TGG	GCT	CCC	CTG	270	Leu
	62															76	
271	AGC	AGC	TGC	CCC	AGC	CAG	GCC	CTG	CAG	CTG	GCA	GGC	TGC	TTG	AGC	315	Ser
	77															91	
316	CAA	CTC	CAT	AGC	GGC	CTT	TTC	CTC	TAC	CAG	GGG	CTC	CTG	CAG	GCC	360	Ala
	92															106	
361	CTG	GAA	GGG	ATC	TCC	CCC	GAG	TTG	GGT	CCC	ACC	TTG	GAC	ACA	CTG	405	Leu
	107															121	
406	CAG	CTG	GAC	GTC	GCC	GAC	TTT	GCC	ACC	ACC	ATC	TGG	CAG	CAG	ATG	450	Met
	122															136	
451	GAA	GAA	CTG	GGA	ATG	GCC	CCT	GCC	CTG	CAG	CCC	ACC	CAG	GGT	GCC	495	Ala
	137															151	
496	ATG	CCG	GCC	TTC	GCC	TCT	GCT	TTC	CAG	CGC	CGG	GCA	GGA	GGG	GTC	540	Val
	152															166	
541	CTA	GTT	GCC	TCC	CAT	CTG	CAG	AGC	TTC	CTG	GAG	GTG	TCG	TAC	CGC	585	Arg
	167															174	
586	GTT	CTA	CGC	CAC	CTT	GCC	CAG	CCC	TAA	TAA						616	
	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	stop	codon							

(see: SEQ ID NO: 18)

(see: SEQ ID NO: 19)

FIG. 3

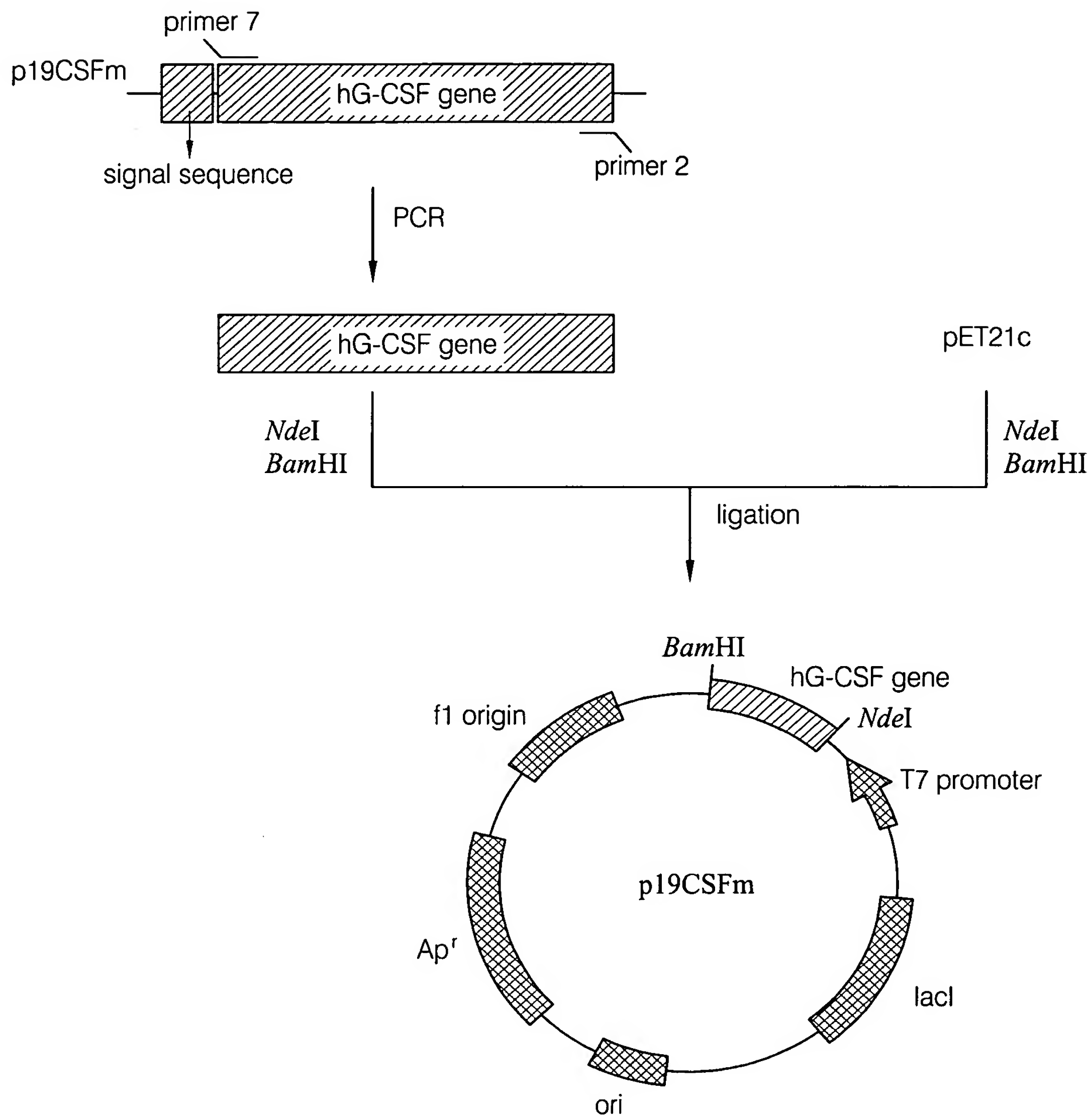


FIG. 4

ESCHERICHIA COLI STRAIN SECRETING HUMAN GRANULOCYTE...

Sang-Yup Lee

Appl. No.: 10/009,792 Atty Docket: HYLEE60.001APC

Replacement Sheet

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1	ATG	ACC	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	15	
1	Met	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	45	
16																30	
46	CTC	AAG	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	90	
	Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala		
31																45	
91	GCG	CTC	CAG	GAG	AAG	CTG	TGT	GCC	ACC	TAC	AAG	CTG	TGC	CAC	CCC	135	
	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro		
46																60	
136	GAG	GAG	CTG	GTG	CTG	CTC	GGA	CAC	TCT	CTG	GGC	ATC	CCC	TGG	GCT	180	
	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala		
61																75	
181	CCC	CTG	AGC	AGC	TGC	CCC	AGC	CAG	GCC	CTG	CAG	CTG	GCA	GGC	TGC	225	
	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys		
76																90	
226	TTG	AGC	CAA	CTC	CAT	AGC	GGC	CTT	TTC	CTC	TAC	CAG	GGG	CTC	CTG	270	
	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu		
91																105	
271	CAG	GCC	CTG	GAA	GGG	ATC	TCC	CCC	GAG	TTG	GGT	CCC	ACC	TTG	GAC	315	
	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp		
106																120	
316	ACA	CTG	CAG	CTG	GAC	GTC	GCC	GAC	TTT	GCC	ACC	ACC	ATC	TGG	CAG	360	
	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln		
121																135	
361	CAG	ATG	GAA	GAA	CTG	GGA	ATG	GCC	CCT	GCC	CTG	CAG	CCC	ACC	CAG	405	
	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln		
136																150	
406	GGT	GCC	ATG	CCG	GCC	TTC	GCC	TCT	GCT	TTC	CAG	CGC	CGG	GCA	GGA	450	
	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly		
151																165	
451	GGG	GTC	CTA	GTT	GCC	TCC	CAT	CTG	CAG	AGC	TTC	CTG	GAG	GTG	TCG	495	
	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser		
166																175	
496	TAC	CGC	GTT	CTA	CGC	CAC	CTT	GCC	CAG	CCC	TAA	TAA				531	
	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	stop	codon					

(see: SEQ ID NO: 20)

(see: SEQ ID NO: 21)

FIG. 5

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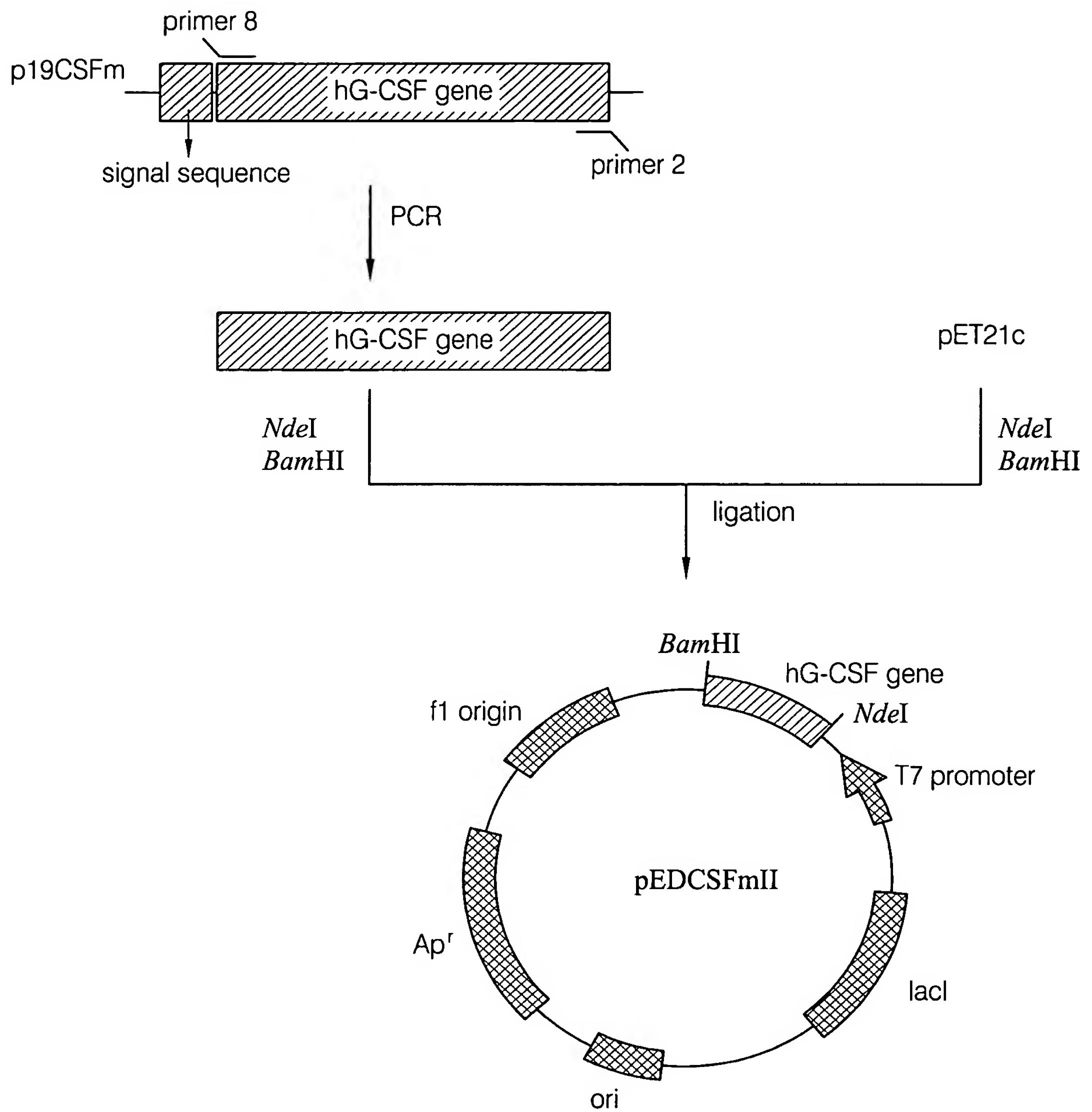


FIG. 6

1	ATG	ACT	CCG	TTA	GGT	CCA	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	45
1	Met	Thr	Pro	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu

(see: SEQ ID NO: 22)

(see: SEQ ID NO: 23)

FIG. 7

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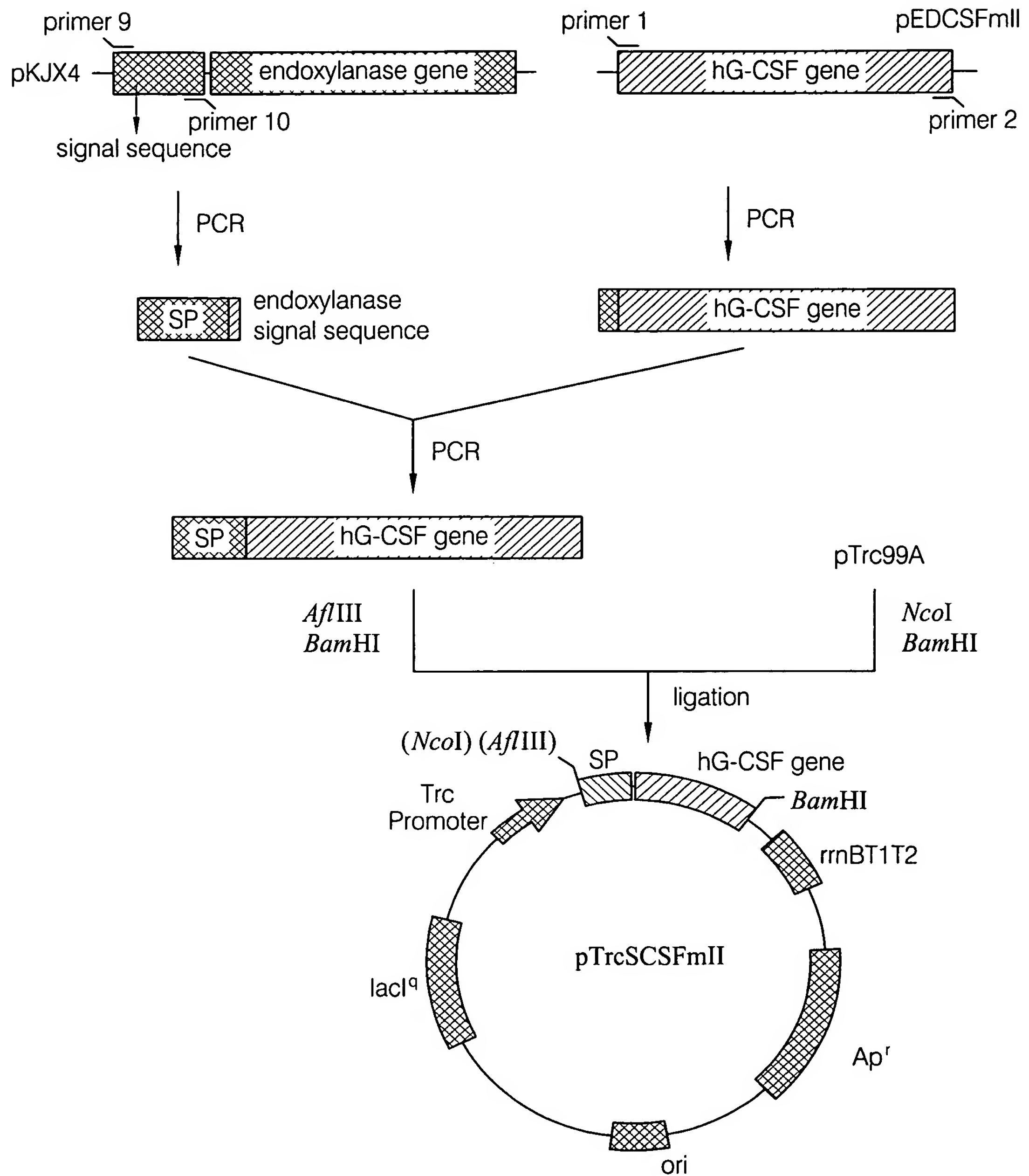


FIG. 8





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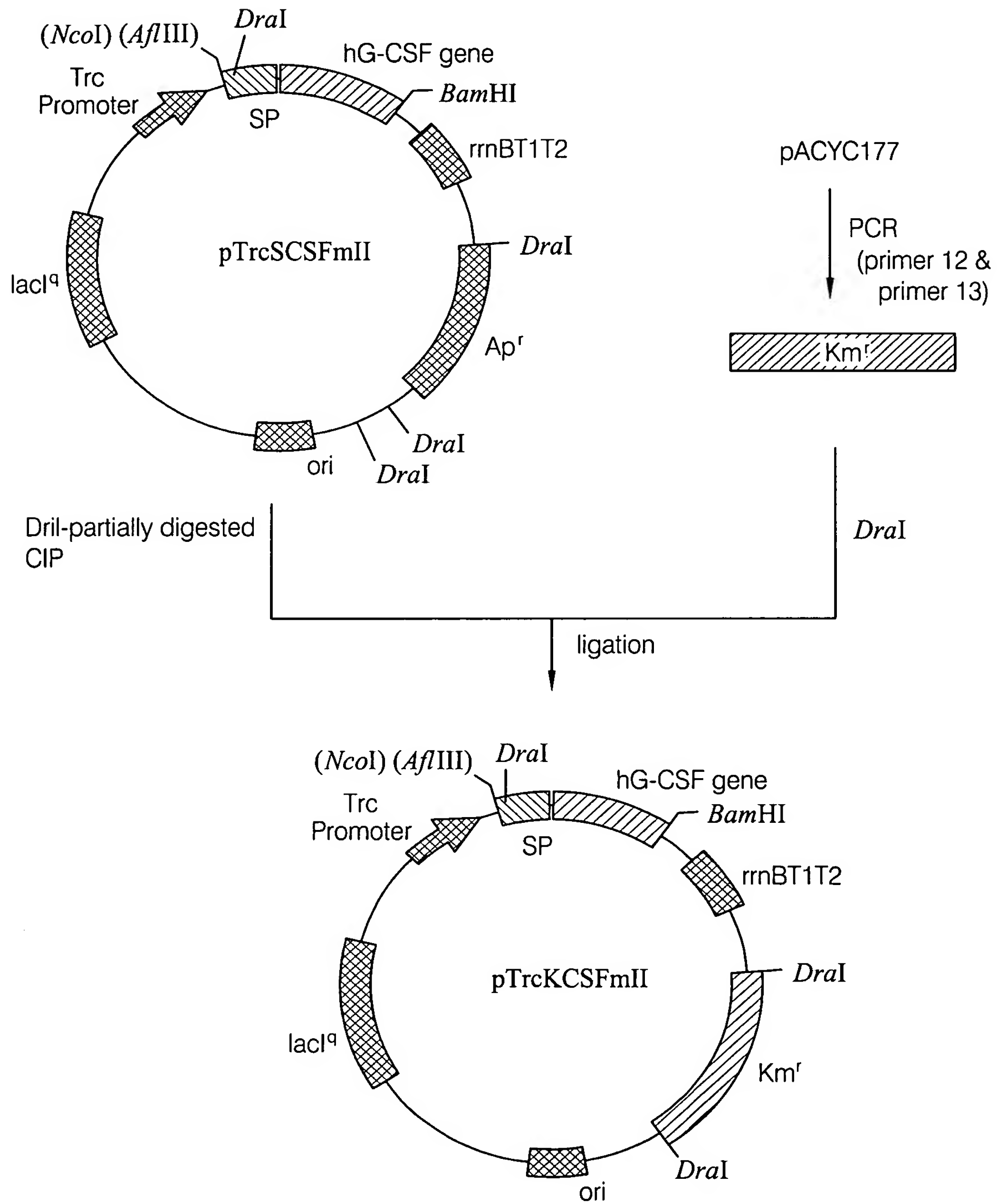


FIG. 10

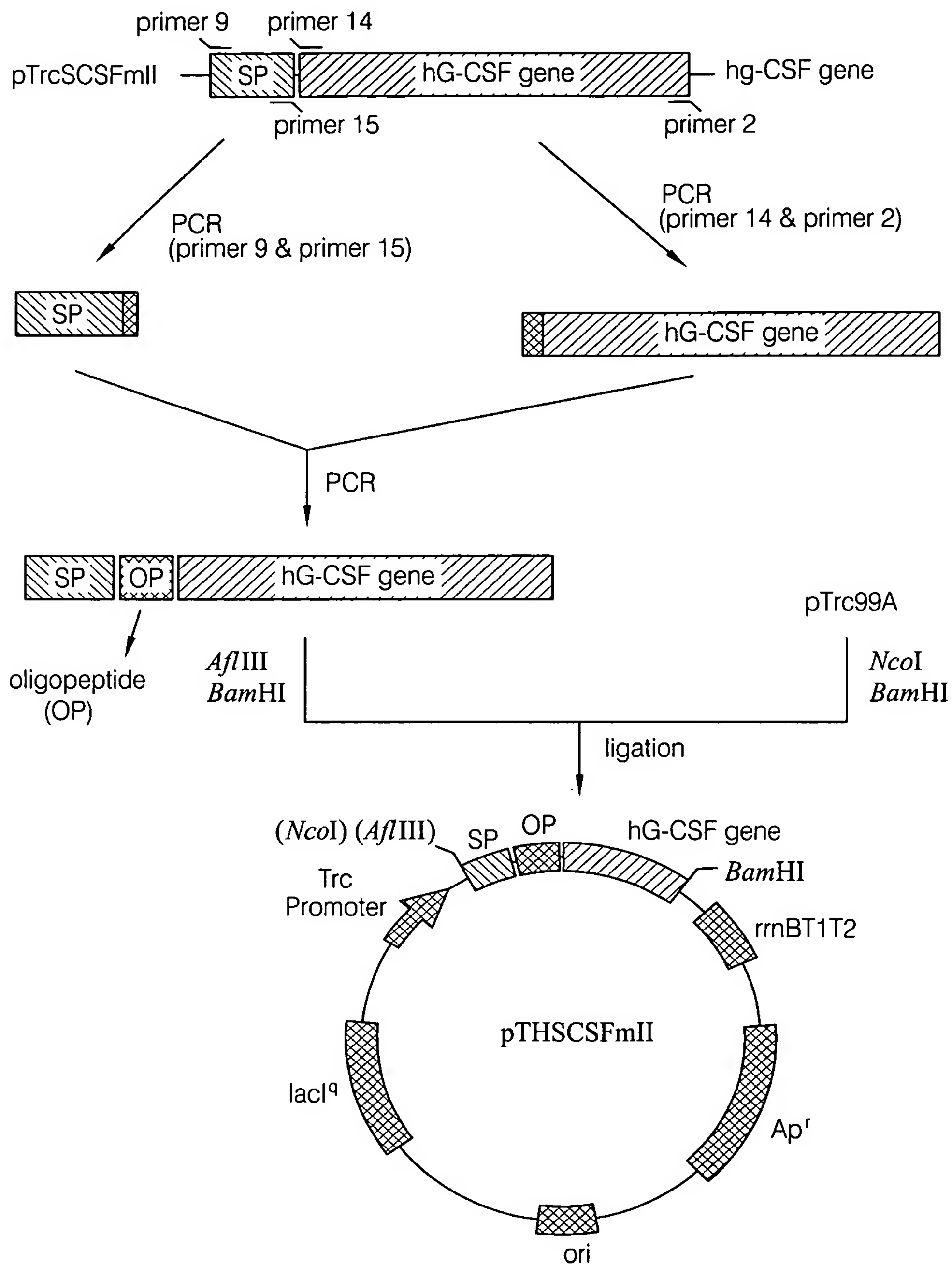


FIG. 11

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1

ATG TTT AAG TTT AAA AAG AAA TTC TTA GTG GGA TTA ACG GCA GCT

Met Phe Lys Phe Lys Lys Lys Phe Phe Leu Val Gly Leu Thr Ala Ala

-1445

-13

46

TTC ATG AGT ATC AGC ATG TTT TCT GCA ACC GCC TCT GCA GCT GGC

Phe Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Ala Gly

-1+1290

3

91

CCG CAC CAT CAC CAT CAC CAT ATC GAG GGA AGG ACT CCG TTA GGT

Pro His His His His His Ile Glu Gly Arg Thr Pro Leu Gly

17135

18

136

CCA GCC AGC TCC CTG CCC CAG AGC TTC CTG CTC AAG TGC TTA GAG

Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu

32180

(see: SEQ ID NO: 26)

(see: SEQ ID NO: 27)

FIG. 12

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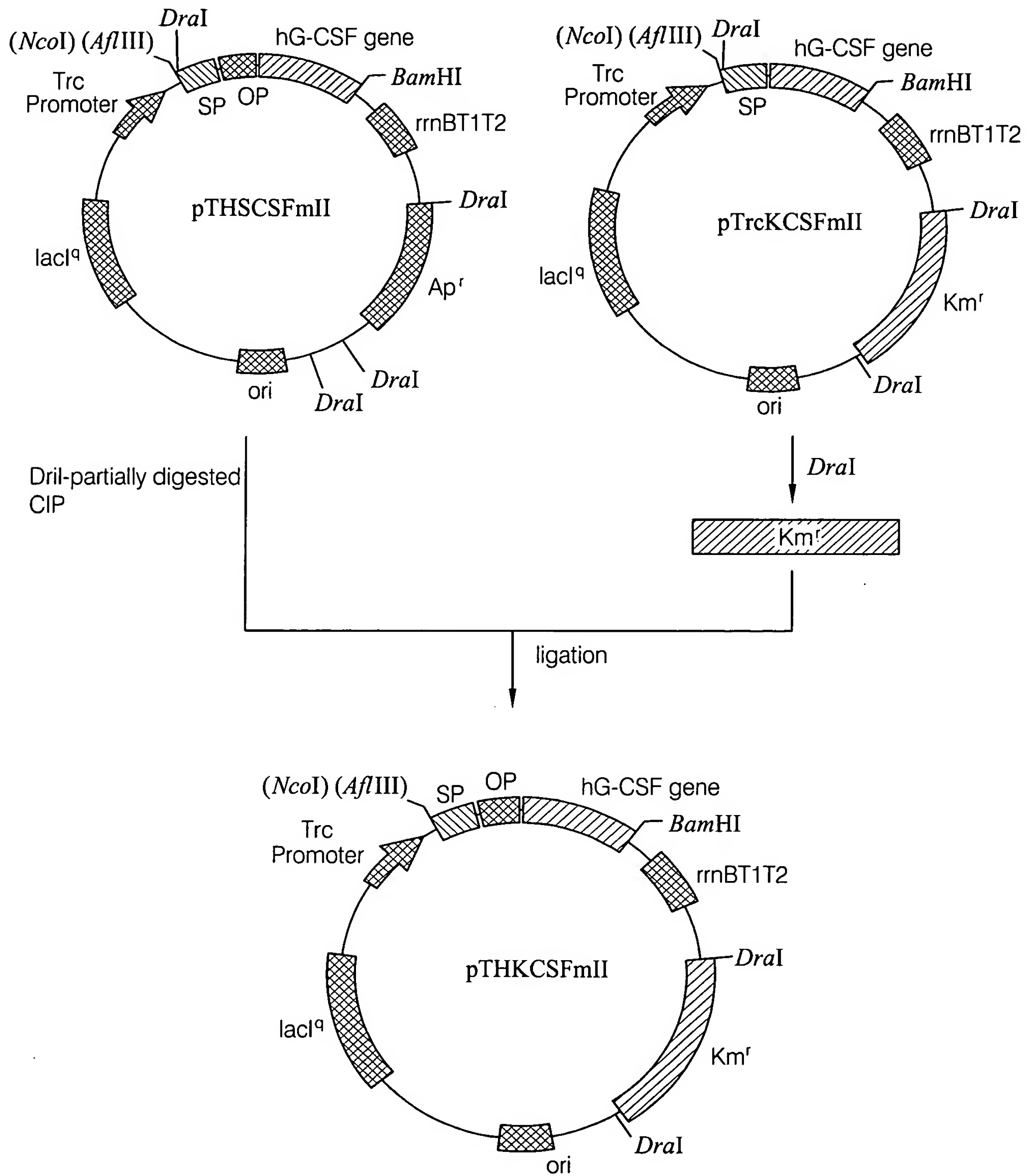


FIG. 13